

Gencore version 4.5
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OM protein - protein search, using sw model.

Run on: March 1, 2001, 16:17:16 ; Search time 52.57 Seconds

(without alignments)
122.626 Million cell updates/sec

Title: US-09-331-631A-25_COPY_31_85

Perfect score: 315

Sequence: 1 ENPKHNCLOCNSERDSVR.....EEEEGETPRPRPRPRQHPER 55

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 374700 seqs, 11720715 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15;*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	RESULT	1	ALIGNMENTS
1	175	55.6	62	10	Q9W402	Q9W402	PRELIMINARY;	PRT;	62 AA.	
2	131	41.6	544	10	Q9W402;	Q9W402;				
3	69.5	22.1	556	5	Q9W402;	Q9W402;				
4	69.5	22.1	556	5	Q9W402;	Q9W402;				
5	67.5	21.4	719	5	Q9W402;	Q9W402;				
6	67	21.3	593	10	Q9W402;	Q9W402;				
7	66.5	21.1	3680	5	Q9W402;	Q9W402;				
8	66	21.0	963	10	Q9W402;	Q9W402;				
9	65.5	20.8	510	5	Q9W402;	Q9W402;				
10	65.5	20.8	774	3	Q9W402;	Q9W402;				
11	64.5	20.5	340	11	Q9W402;	Q9W402;				
12	64.5	20.5	704	13	Q9W402;	Q9W402;				
13	63.5	20.2	414	5	Q9W402;	Q9W402;				
14	63	20.0	663	5	Q9W402;	Q9W402;				
15	62.5	19.8	519	2	Q9W402;	Q9W402;				
16	62.5	19.8	3767	5	Q9W402;	Q9W402;				
17	62	19.7	190	10	Q9W402;	Q9W402;				
18	62	19.7	190	10	Q9W402;	Q9W402;				
19	62	19.7	238	10	Q9W402;	Q9W402;				

20	62	19.7	244	10	Q9SJD9	Q9SJD9	arabidopsis			
21	62	19.7	255	10	Q9S081	Q9S081	arabidopsis			
22	62	19.7	462	10	Q93249	Q93249	arabidopsis			
23	62	19.7	607	5	Q9V657	Q9V657	drosophila			
24	62	19.7	807	13	Q9IA01	Q9IA01	ictalurus p			
25	61.5	19.5	191	10	Q9SH2	Q9SH2	arabidopsis			
26	61	19.4	147	5	Q9U055	Q9U055	caenorhabdi			
27	61	19.4	190	10	Q9SBH5	Q9SBH5	arabidopsis			
28	61	19.4	472	10	Q9SH43	Q9SH43	arabidopsis			
29	61	19.4	757	5	Q9VZP2	Q9VZP2	drosophila			
30	61	19.4	1952	3	Q9P6T1	Q9P6T1	neurospora			
31	60.5	19.4	600	4	Q95402	Q95402	homo sapien			
32	60.5	19.2	2277	5	Q9U055	Q9U055	plasmid			
33	60	19.0	68	11	Q70562	Q70562	mus musculus			
34	60	19.0	190	10	Q9SBH0	Q9SBH0	arabidopsis			
35	60	19.0	1132	4	P78418	P78418	homo sapien			
36	59.5	18.9	1101	4	Q9XV9	Q9XV9	homo sapien			
37	59	18.9	76	11	Q70556	Q70556	mus musculus			
38	59	18.7	190	10	Q9SBH6	Q9SBH6	arabidopsis			
39	59	18.7	190	10	Q9SBH4	Q9SBH4	arabidopsis			
40	59	18.7	190	10	Q9SBH1	Q9SBH1	arabidopsis			
41	59	18.7	190	10	Q9SBG8	Q9SBG8	arabidopsis			
42	59	18.7	190	10	Q9ST80	Q9ST80	arabidopsis			
43	59	18.7	190	10	Q9S779	Q9S779	arabidopsis			
44	59	18.7	199	5	P91512	P91512	caenorhabdi			
45	59	18.7	281	5	Q23778	Q23778	chironomus			

Query Match 22.1%; Score 69.5; DB 5; Length 556; Best Local Similarity 33.3%; Pred. No. 1.2; Matches 18; Conservative 4; Mismatches 23; Indels 9; Gaps 2;

01-JAN-1998 (TREMBLrel. 05, Last sequence update) DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update) DT SUBUNIT OF BETA CONGLYCININ. DE GLYCINE MAX (Soybean) OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine. OC NCBI_TaxID=3847; OC RN [1] RP SEQUENCE FROM N.A. STRAIN=CV. WASESIZUNARI; RA Maruyama N., Katsube T., Wada Y., Utsunomi S.; RL Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases. DR EMBL; AB008678; BAA23360.1; -. DR HSSP; P50477; ICANU. DR MENDL; 25074; Glyma-1188-25074. DR INTERPRO; IPR001113; -. DR PFAM; PF00546; Seedstore_7s; 1. DR PDOM; PF081059; -. DR SEQUENCE 544 AA; 63296 MW; 048B243929A9C9AB CRC64; SQ

Query Match 41.6%; Score 131; DB 10; Length 544; Best Local Similarity 100.0%; Pred. No. 4.5e-08; Mismatches 0; Indels 0; Gaps 0; RT Matches 23; Conservative 23; Indels 0; Gaps 0; QY 33 VERKECEGEIGIRRPRPQHPER 55 Db 2 VERKECEGEIGIRRPRPQHPER 24

RESULT 3 096456 ID 096456 PRELIMINARY; PRT; 556 AA. AC 096456: DT 01-MAY-1999 (TREMBLrel. 10, Created) 01-MAY-1999 (TREMBLrel. 10, Last sequence update) 01-MAY-1999 (TREMBLrel. 10, Last annotation update) DE SPOROZOITE SURFACE PROTEIN 2. DR HSSP; P50477; ICANU. DR MENDL; 25074; Glyma-1188-25074. DR INTERPRO; IPR00035; -. DR PFAM; PF00080; tsp_1; 1. DR PRINTS; PR00453; VWFA DOMAIN. DR FT VARIANT 134 134 D -> E. DR FT VARIANT 160 160 V -> I. DR FT VARIANT 166 166 R -> T. DR FT VARIANT 172 172 N -> K. DR FT VARIANT 268 268 K -> G. DR FT VARIANT 352 352 D -> E. DR FT VARIANT 391 391 M -> R. DR FT VARIANT 464 464 E -> Q. DR SEQUENCE 556 AA; 61208 MW; 7FAEB294B3E32AA7 CRC64; OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. OC NCBI_TaxID=5855; [1] RN RP SEQUENCE FROM N.A. RC STRAIN=SA1; RA Rogers W.O., Gowda K., Hoffman S.L.; RT Construction and immunogenicity of DNA vaccine plasmids encoding four Plasmodium vivax candidate vaccine antigens. " Vaccine 17:3136-3144(1999). DR EMBL; AF063137; AAC91485.1; -. DR INTERPRO; IPR000884; -. DR PDOM; PF00080; tsp_1; 1. DR PRINTS; PR00453; VWFA DOMAIN. DR FT VARIANT 134 134 D -> E. DR FT VARIANT 160 160 V -> I. DR FT VARIANT 166 166 R -> T. DR FT VARIANT 172 172 N -> K. DR FT VARIANT 268 268 K -> G. DR FT VARIANT 352 352 D -> E. DR FT VARIANT 391 391 M -> R. DR FT VARIANT 464 464 E -> Q. DR SEQUENCE 556 AA; 61208 MW; 7FAEB294B3E32AA7 CRC64; OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. OC NCBI_TaxID=5855; [1] RN RP SEQUENCE FROM N.A. RC STRAIN=SA1; RA Rogers W.O., Gowda K., Hoffman S.L.; RT Construction and immunogenicity of DNA vaccine plasmids encoding four Plasmodium vivax candidate vaccine antigens. " Vaccine 17:3136-3144(1999). DR EMBL; AF063136; AAC91484.1; -. DR INTERPRO; IPR000884; -. DR PDOM; PF00080; tsp_1; 1. DR PRINTS; PR00453; VWFA DOMAIN. DR FT VARIANT 134 134 D -> E. DR FT VARIANT 160 160 V -> I. DR FT VARIANT 166 166 R -> T. DR FT VARIANT 172 172 N -> K. DR FT VARIANT 268 268 K -> G. DR FT VARIANT 352 352 D -> E. DR FT VARIANT 391 391 M -> R. DR FT VARIANT 464 464 E -> Q. DR SEQUENCE 556 AA; 61208 MW; 7FAEB294B3E32AA7 CRC64; OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. OC NCBI_TaxID=5855; [1] RN RP SEQUENCE FROM N.A. RC STRAIN=BERKELEY; MEDLINE=20196005; PubMed=10731132; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanaiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Query Match 22.1%; Score 69.5; DB 5; Length 556; Best Local Similarity 33.3%; Pred. No. 1.2; Matches 18; Conservative 4; Mismatches 23; Indels 9; Gaps 2;

01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update) DT SEQUENCE FROM N.A. STRAIN=BERKELEY; MEDLINE=20196005; PubMed=10731132; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanaiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

QY 8 CLOSCNSERDSYRNQACHARCNLJKVKEECEGE-----IPRPRPRPQHPE 54 Db 249 CSVTCGRTHSRSRPSLHEKCTHMY--SCEBEGCPVEPEPLPVAPLPLVPE 300

RESULT 4 09W4BB ID 09W4BB PRELIMINARY; PRT; 719 AA. AC 09W4BB; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update) DE CG3239 PROTEIN. GN CG3239. DR Drosophila melanogaster (Fruit fly). OS Drosophila melanogaster (Fruit fly). OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydriidea; Drosophilidae; Drosophila. OC NCBI_TaxID=7227; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=BERKELEY; MEDLINE=20196005; PubMed=10731132; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanaiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.-A., Ye J., Yeh J.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of <i>Drosophila melanogaster</i> ."; Science 287:2185-2195(2000).	Q94727	PRELIMINARY;	PRT;	510 AA.
RA	HSSP; P35555; 1ENN.	Q94727			
RA	PROTEIN; IPR000152; -.	01-FEB-1997 (TREMBLrel. 02, Created)			
RT	"The genome sequence of <i>Drosophila melanogaster</i> .";	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
RL	Science 287:2185-2195(2000).	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DR	EMBL; AE003576; AAF51000.1; -.	DE THROMBOSPONDIN-RELATED ANONYMOUS PROTEIN (FRAGMENT).			
DR	HSSP; P35555; 1ENN.	TRAP.			
DR	FIBBASE; FFBN0031612; CG15637.	Plasmodium vivax.			
DR	INTERPRO; IPR000152; -.	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
DR	INTERPRO; IPR000561; -.	OX NCBI_TAXID=5855;			
DR	INTERPRO; IPR001881; -.	RN [1]			
DR	PFAM; PF00008; EGF; 28.	RP SEQUENCE FROM N.A.			
DR	PROSITE; PS00010; AXS_HYDROXYL; 18.	RC STRAIN=SAL-1;			
DR	PROSITE; PS00022; EGF_1; 1.	RX MEDLINE=97193932; PubMed=9041517;			
DR	PROSITE; PS01186; EGF_2; 18.	RA Templeton T.J., Kaslow D.C.;			
DR	PROSITE; PS01187; EGF_CA; 17.	RT "Cloning and cross-species comparison of the thrombospondin-related anonymous protein (TRAP) gene from <i>Plasmodium knowlesi</i> , <i>Plasmodium vivax</i> and <i>Plasmodium gallinaceum</i> .";			
SQ	SEQUENCE 3680 AA; 388637 MW; E5E972E1A3479EFF CRC64;	RT Mol. Biochem. Parasitol. 84:13-24 (1997).			
Db	2878 PQ 2879	RL EMBL; U64901; AAC4743.1; -.			
RESULT	8	DR INTERPRO; IPR000884; -.			
Q9M8T1	PRELIMINARY;	DR PFAM; PF00092; vwa; 1.			
ID	Q9M8T1	PRINTS; PR00453; WVFADOMAIN.			
AC	Q9M8T1; 1;	FT NON_TER 1			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	FT NON_TER 510 AA; 55601 MW; 72687C7BAFDA41D CRC64;			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)				
DE	F13E7_16 PROTEIN.				
GN					
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Embryophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
OC	NCBI_TAXID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC					
RA	Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M., "Arabidopsis thaliana chromosome III BAC F13E7 genomic sequence."; Submitted (JAN 2000) to the EMBL/GenBank/DDBJ databases.	Query Match Best Local Similarity 21.0%; Score 66; DB 5; Length 510; Matches 21; Conservative 3; Mismatches 13; Indels 28; Gaps 3;	Q94727	PRELIMINARY;	PRT;
RA	DR EMBL; AC018363; AAF26970.1; -.	Q94727 PRELIMINARY; PRT; 510 AA.			
SO	SEQUENCE 963 AA; 105391 MW; D2041DC04280339 CRC64;	AC 042913;			
Qy	1 ENPKHKL-----OSCNSRSRSYRNQACHARCNLLKVEKE-----EC 38	DT 01-JAN-1999 (TREMBLrel. 09, Created)			
Db	832 ENPKHKL-----OSCNSRSRSYRNQACHARCNLLKVEKE-----EC 38	DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)			
Qy	39 EEGET 43	DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
Db	886 EEEGET 890	DE PUTATIVE ALPHA-AMYLASE C16A3.13 PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE).			
		GN SPBC16A3.13.			
		OS Schizosaccharomyces pombe (Fission yeast).			
		OC Eukaryota; Ascomycota; Schizosaccharomyces; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.			
		OC NCBI_TAXID=4897;			
		RN [1]			
		RP SEQUENCE FROM N.A.			
		RC STRAIN=972;			
		RA Wood V., Rajandream M.A., Barrell B.G., Beck A., Reinhardt R.; RL Submitted (FEB 1998) to the EMBL/GenBank/DDBJ databases.			
		CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.			
		CC -!- COFACTOR: Binds A CALCIUM ION REQUIRED FOR ITS ACTIVITY (BY SIMILARITY).			
		CC -!- SIMILARITY: TO THE FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.			
		DR EMBL; AL01748; CAA16864.1; -.			
		DR HSSP; P10529; TPA.			
		DR INTERPRO; IPR000461; -.			
		DR PFAM; PF00128; alpha-amylase; 1.			
		KW Hypothetical protein; Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Glycoprotein; Signal.			
		FT SIGNAL 1 24 POTENTIAL.			
		CHAIN 25 774 PUTATIVE ALPHA-AMYLASE C16A3.13.			
RESULT	9				

FT	ACT SITE	461	461	BY SIMILARITY.	GN	HGF1/MSP.
FT	ACT-SITE	553	553	BY SIMILARITY.	OS	Galius galius (Chicken).
FT	DISULFID	52	60	BY SIMILARITY.	OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
FT	DISULFID	229	314	BY SIMILARITY.	OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
FT	DISULFID	495	539	BY SIMILARITY.	OC	Galius.
FT	DISULFID	690	724	BY SIMILARITY.	OX	NCBI_TAXID:9031;
FT	CARBOHYD	143	143	POTENTIAL.	RN	11;
FT	CARBOHYD	187	187	POTENTIAL.	RP	SEQUENCE FROM N.A.
FT	CARBOHYD	214	214	POTENTIAL.	RC	TISSUE-LIVER;
FT	CARBOHYD	243	243	POTENTIAL.	RX	Medline=9602910; PubMed=7554499;
FT	CARBOHYD	272	272	POTENTIAL.	RA	Theory C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi E.;
FT	CARBOHYD	299	299	POTENTIAL.	RT	"Expression of HGF/SF, HGF/MSP, and c-met suggests new functions
FT	CARBOHYD	326	326	POTENTIAL.	RT	during early chick development.;"
FT	CARBOHYD	355	355	POTENTIAL.	RL	Dev. Genet. 17:90-101(1995);
FT	CARBOHYD	382	382	POTENTIAL.	DR	EMBL; X84043; CAA58862.1; -.
FT	CARBOHYD	409	409	POTENTIAL.	DR	HSPP; P00747; ICER.
SQ	SEQUENCE	774 AA;	89459 MW;	92CEAAE45664269B CRC64;	DR	MEROPS; S01_977; -.
Query	Match	20.8%	Score 65.5;	DB 3;	DR	INTERPRO; IPR001254; -.
Best	Local Similarity	28.1%	Pred. No. 5;	Length 774;	DR	INTERPRO; IPR03314; -.
Matches	16;	Conservative	8;	Mismatches 20;	DR	INTERPRO; IPR003014; -.
QY	6	NKCLQCSNSERDSYRNQACHARCNLLKVE-----KECEEEGIPRPRPRP---RPOH	52	Indels 13;	DR	PFAM; PF00024; PAN; 1.
Db	167	HKCKEKEHCSCHHDKPRPVPH--NGTKRDPDKPKWPKHEBCHGKPRPVPHNGTKPDH	220	Gaps 3;	DR	PFAM; PF00051; KRingle; 4.
RESULT	11				DR	PRINTS; PRO0018; KRNGL; 1.
ID	008641	PRELIMINARY;	PRN;	340 AA.	DR	PRINTS; PR0072; CHYMOTRYPSIN.
ID	008641;				DR	PROSITE; PS0021; KRINGLE; 1; UNKNOWN-4.
AC					DR	SEQUENCE 704 AA; 79341 MW; CAB08CC41367C37 CRC64;
DT	01-JUL-1997	(TREMBLrel. 04, Created)			DR	INTERPRO; IPR000001; -.
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)			DR	INTERPRO; IPR00314; -.
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)			DR	INTERPRO; IPR003014; -.
DE					DR	INTERPRO; IPR000001; -.
GN					DR	INTERPRO; IPR001254; -.
OS					DR	INTERPRO; IPR03314; -.
OC					DR	INTERPRO; IPR003014; -.
OX					DR	INTERPRO; IPR00051; KRingle; 4.
RN					DR	PRINTS; PRO0018; KRNGL; 1.
RP					DR	PRINTS; PR0072; CHYMOTRYPSIN.
RC					DR	PROSITE; PS0021; KRINGLE; 1; UNKNOWN-4.
RA					DR	SEQUENCE 704 AA; 79341 MW; CAB08CC41367C37 CRC64;
RL					DR	INTERPRO; IPR000001; -.
Submitted	(JUN-1996)	to the EMBL/GenBank/DBJ databases.			DR	INTERPRO; IPR001254; -.
DR	D85926;	BAI19679.1; -.			DR	INTERPRO; IPR03314; -.
DR	P29354;	1GRC.			DR	INTERPRO; IPR003014; -.
DR	MGI; MGJ:	1346118; Sh3yl1.			DR	INTERPRO; IPR000001; -.
DR	INTERPRO;	IPR001452; -.			DR	INTERPRO; IPR001254; -.
DR	PFAM;	PF00018; SH3; 1.			DR	INTERPRO; IPR03314; -.
DR	PRINTS;	PR00452; SH3DOMAIN.			DR	INTERPRO; IPR003014; -.
DR	PROSITE;	PS00022; SH3; 1.			DR	INTERPRO; IPR00051; KRingle; 4.
SQ	SEQUENCE FROM N.A.				DR	PRINTS; PRO0018; KRNGL; 1.
SPRAIN-C57BL6; TISSUE=SKIN;					DR	SEQUENCE 704 AA; 79341 MW; CAB08CC41367C37 CRC64;
Aoki N.;					DR	INTERPRO; IPR000001; -.
Submitted	(JUN-1996)	to the EMBL/GenBank/DBJ databases.			DR	INTERPRO; IPR001254; -.
DR	D85926;	BAI19679.1; -.			DR	INTERPRO; IPR03314; -.
DR	P29354;	1GRC.			DR	INTERPRO; IPR003014; -.
DR	MGI; MGJ:	1346118; Sh3yl1.			DR	INTERPRO; IPR000001; -.
DR	INTERPRO;	IPR001452; -.			DR	INTERPRO; IPR001254; -.
DR	PFAM;	PF00018; SH3; 1.			DR	INTERPRO; IPR03314; -.
DR	PRINTS;	PR00452; SH3DOMAIN.			DR	INTERPRO; IPR003014; -.
DR	PROSITE;	PS00022; SH3; 1.			DR	INTERPRO; IPR00051; KRingle; 4.
SQ	SEQUENCE	340 AA;	37028 MW;	3FE12C0A8530C74E CRC64;	DR	PRINTS; PRO0018; KRNGL; 1.
RESULT	13				DR	SEQUENCE 704 AA; 79341 MW; CAB08CC41367C37 CRC64;
ID	Q0155	PRELIMINARY;	PRN;	414 AA.	DR	INTERPRO; IPR000001; -.
ID	Q20155	PRELIMINARY;	PRN;	414 AA.	DR	INTERPRO; IPR001254; -.
AC	Q20155;				DR	INTERPRO; IPR03314; -.
AC	Q20155;				DR	INTERPRO; IPR003014; -.
DT	01-NOV-1996	(TREMBLrel. 01, Created)			DR	INTERPRO; IPR000001; -.
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)			DR	INTERPRO; IPR001254; -.
DT	01-JUN-2000	(TREMBLrel. 14, Last annotation update)			DR	INTERPRO; IPR03314; -.
DE	F38B7.1 PROTEIN.				DR	INTERPRO; IPR003014; -.
GN	F38B7.1				DR	INTERPRO; IPR00051; KRingle; 4.
OS	Caenorhabditis elegans.				DR	INTERPRO; IPR000001; -.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				DR	INTERPRO; IPR001254; -.
OC	Rhabditidae; Peioderinae; Caenorhabditis.				DR	INTERPRO; IPR03314; -.
OC	NCBI_TAXID:6239;				DR	INTERPRO; IPR003014; -.
RN	[1]				DR	INTERPRO; IPR000001; -.
SEQUENCE FROM N.A.					DR	INTERPRO; IPR001254; -.
RN	Leonard N.;				DR	INTERPRO; IPR03314; -.
RN					DR	INTERPRO; IPR003014; -.
RA					DR	INTERPRO; IPR000001; -.
RA					DR	INTERPRO; IPR001254; -.
RA					DR	INTERPRO; IPR03314; -.
RA					DR	INTERPRO; IPR003014; -.
RL					DR	INTERPRO; IPR000001; -.
RL					DR	INTERPRO; IPR001254; -.
RL					DR	INTERPRO; IPR03314; -.
RL					DR	INTERPRO; IPR003014; -.
CC	-1- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED BY				DR	INTERPRO; IPR000001; -.
CC	ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN IS THAT				DR	INTERPRO; IPR001254; -.
CC	OF FORM A.				DR	INTERPRO; IPR03314; -.
CC	OF FORM B.				DR	INTERPRO; IPR003014; -.
EMBL	Z74033; CA98475.1;				DR	INTERPRO; IPR000001; -.
EMBL	Z74033; CA98476.1;				DR	INTERPRO; IPR001254; -.
EMBL	Z74033; CA98476.1;				DR	INTERPRO; IPR03314; -.
EMBL	Z74033; CA98476.1;				DR	INTERPRO; IPR003014; -.
DR	INTERPRO; IPR000571; -.				DR	INTERPRO; IPR000001; -.
DR	PF00642; zf-CCHC; 2.				DR	INTERPRO; IPR001254; -.
KW	Hypothetical protein; Alternative splicing.				DR	INTERPRO; IPR03314; -.
FT	VARSPIC 1				DR	INTERPRO; IPR003014; -.
FT	VARSPIC 39				DR	INTERPRO; IPR000001; -.
FT	VARSPIC 52				DR	INTERPRO; IPR001254; -.
FT	VARSPIC B.				DR	INTERPRO; IPR03314; -.
FT	VARSPIC B.				DR	INTERPRO; IPR003014; -.
SQ	SEQUENCE	414 AA;	44308 MW;	D8B29D29A9E39583 CRC64;	DR	INTERPRO; IPR000001; -.
QY	13	NSERDSVNRQACHARCLLKVKEECEGEGEL-PRP--RPRQHP	53		DR	INTERPRO; IPR001254; -.
QY	208	NSFTEKVETEG--QRINLKVAREQRKAKELPPKSSRPQPAHP	249		DR	INTERPRO; IPR03314; -.
Db					DR	INTERPRO; IPR003014; -.
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Db			</			

OX NCBI_TAXID:1313;
 RN [1]
 RP
 RC
 STRAIN:G99;
 RA Iannelli F., Oggioni M.R., Spinoza M.R., Pozzi G.;
 RT "Allelic variants of surface protein PspC (SpsA, CbpA, PbcA) of
 Streptococcus pneumoniae.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 DR AP154036; AAF73808.1; -.
 EMBL; AP154036; AAF73808.1; -.
 SRQENCE 519 AA: 58731 MW: 7E1875958254RDLE CRC64
 SQ

RESULT 14
 62446 PRELIMINARY; PRT; 663 AA.
 D 062446; PRELIMINARY; PRT; 663 AA.
 C 062446;
 T 01-AUG-1998 ("TREMBLrel. 07, Created")
 T 01-AUG-1998 ("TREMBLrel. 07, Last sequence update")
 T 01-MAY-2000 ("TREMBLrel. 13, Last annotation update")
 E Y43F4A.1 PROTEIN.
 N Y43F4A.1.
 S Caenorhabditis elegans.
 C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Pelioderinida; Caenorhabditis.

[1]
N P P
SEQUENCE FROM N.A.
A
Matthews L.;
L Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

Search completed: March 1, 2001, 16:17:18
Job time: 456 sec

Query Match 20.0%; Score 53; DB 5; Length 663; .
 Best Local Similarity 35.9%; Pred. No. 8.8; .
 Matches 14; Conservative 4; Mismatches 17; Indels 4; Gaps 1;

121 KCISFFYYKQGMNVACDKGCR-----ERTTCGEADIPR 155

01-OCT-2000 (TREMBLrel. 15, Created)
 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 SURFACE PROTEIN_PSPCR

Bacterium: Firmicutes; *Bacillus/Clostridium* group; *Streptococcaceae*; *Streptococcus*.